



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/720,896
Source: IFW
Date Processed by STIC: 12/16/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/720,896

DATE: 12/16/2003

TIME: 17:13:14

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\12112003\J720896.raw

3 <110> APPLICANT: Solari, Roberto Celeste Ercole
 4 Champion, Brian Robert
 5 Ward, George Albert
 7 <120> TITLE OF INVENTION: Conjugate of a Transport Protein and a Protein for
 Modulation

8 of Notch Signalling
 10 <130> FILE REFERENCE: 674525-2007

C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/720,896

C--> 13 <141> CURRENT FILING DATE: 2003-11-24

15 <150> PRIOR APPLICATION NUMBER: 2002-05-24

W--> 16 <151> PRIOR FILING DATE: PCT/GB02/02438

18 <150> PRIOR APPLICATION NUMBER: 2001-05-25

W--> 19 <151> PRIOR FILING DATE: GB 0112818.0

21 <160> NUMBER OF SEQ ID NOS: 13

23 <170> SOFTWARE: PatentIn version 3.1

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 29

27 <212> TYPE: DNA

28 <213> ORGANISM: Artificial sequence

W--> 29 <220> FEATURE: please remove, not needed.W--> 30 <221> NAME/KEY: PCR primer for amplifying HES1 promoter from mouse genomic DNAW--> 32 <223> OTHER INFORMATION: ← please move <221> response to <223> section. please

W--> 32 <400> 1

33 ggggtaccct caggegcgcgcg ccattggcc

36 <210> SEQ ID NO: 2

37 <211> LENGTH: 29

38 <212> TYPE: DNA

39 <213> ORGANISM: Artificial sequence

41 <220> FEATURE: please remove, not needed.W--> 42 <221> NAME/KEY: PCR primer for amplifying HES1 promoter from mouse genomic DNAW--> 44 <223> OTHER INFORMATION: ← please move <221> response to <223> section. please

W--> 44 <400> 2

45 gaagatctgc ttacgtcctt ttacttgac

48 <210> SEQ ID NO: 3

49 <211> LENGTH: 26

50 <212> TYPE: DNA

51 <213> ORGANISM: Artificial sequence

W--> 52 <220> FEATURE: please remove, not needed.W--> 53 <221> NAME/KEY: Adenovirus major late promoter TATA-box motif with BglIII andW--> 54 HindIII cohesive endsW--> 56 <223> OTHER INFORMATION: ← please move <221> response to <223> section.

W--> 56 <400> 3

57 gatctggggg gctataaaag ggggta

60 <210> SEQ ID NO: 4

**Does Not Comply
 Corrected Diskette Needed**
 (pg. 1-3)
 A response for section 2237 Artificial sequence on Genus/Species is mandatory, if

see pg. 6 For error explanation.²⁹

see pg. 6 For error explanation.²⁹

see pg. 6 For error explanation.²⁶

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Input Set : A:\Sequence Listing.txt

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```

61 <211> LENGTH: 26
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial sequence
W--> 64 <220> FEATURE: please remove, not needed,
W--> 65 <221> NAME/KEY: Adenovirus major late promoter TATA-box motif with BglII and
W--> 66 HindIII cohesive ends
W--> 68 <223> OTHER INFORMATION: move to
W--> 68 <400> 4 same error
69 acccccccgat attttccccc attcga 26
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 61
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial sequence
W--> 76 <220> FEATURE: please remove, not needed,
W--> 77 <221> NAME/KEY: CBF-1 promoter tetramer with XhoI and BglII cohesive ends
W--> 79 <223> OTHER INFORMATION: move to
W--> 79 <400> 5 same error
80 tcgagaccgt gggaacttaa ccgtgggaac ttaaccgtgg gaacttaacc gtgggaactt 60
82 a 61
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 61
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial sequence
W--> 89 <220> FEATURE: please remove, not needed,
W--> 90 <221> NAME/KEY: CBF-1 promoter tetramer with XhoI and BglII cohesive ends
W--> 92 <223> OTHER INFORMATION: move to
W--> 92 <400> 6 same error
93 ctggcaccct tgaattggca cccttgaatt ggcacccttg aattggcacc cttgaatcta 60
95 g 61
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 39
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial sequence
W--> 102 <220> FEATURE: please remove, not needed,
W--> 103 <221> NAME/KEY: PCR amplimer for generating a truncated fragment of human
W--> 104 Notch1 cDNA
W--> 106 <223> OTHER INFORMATION: move to
W--> 106 <400> 7 same error
107 aaaggatcca ccatggcacg caagcgccgg cgcagtcatt 39
110 <210> SEQ ID NO: 8
111 <211> LENGTH: 31
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial sequence
W--> 114 <220> FEATURE: please remove, not needed,
W--> 115 <221> NAME/KEY: PCR amplimer for generating a truncated fragment of human
W--> 116 Notch1 cDNA
W--> 118 <223> OTHER INFORMATION: move to
W--> 118 <400> 8 same error
119 ggcctcgag ttagtcacg ggcgagagca t 31

```

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Input Set : A:\Sequence Listing.txt

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```

122 <210> SEQ ID NO: 9
123 <211> LENGTH: 91
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial sequence
W--> 126 <220> FEATURE: please remove, not needed.
W--> 127 <221> NAME/KEY: Oligo annealed to the NIC2202 sequence to remove the stop
W--> 128 codon from theNIC2202 fragment of human Notch1 cDNA
W--> 130 <223> OTHER INFORMATION: move to same error
W--> 130 <400> 9
131 cctggcctgt ggaagcaagg aggccaagga cctcaaggca cggaggaaga agtcccagga 60
133 tggcaagggc tgcctgctgg acggcggccg c 91
136 <210> SEQ ID NO: 10
137 <211> LENGTH: 95
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial sequence
141 <220> FEATURE: please remove, not needed.
W--> 142 <221> NAME/KEY: Oligo annealed to the NIC2202 sequence to remove the stop
W--> 143 codon from theNIC2202 fragment of human Notch1 cDNA
W--> 145 <223> OTHER INFORMATION: move to same error
W--> 145 <400> 10
146 ggaccggaca ccttcgttcc tccggttcc tggagttccgt gcttccttct tcagggtcct 60
148 accgttcccg acggacgacc tgccgcggcg gagct 95
151 <210> SEQ ID NO: 11
152 <211> LENGTH: 2556
153 <212> TYPE: PRT
154 <213> ORGANISM: Homo sapiens
156 <220> FEATURE:
157 <221> NAME/KEY: MISC FEATURE
158 <222> LOCATION: (891)..(892)
159 <223> OTHER INFORMATION: x = any amino acid
162 <400> SEQUENCE: 11
164 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
165 1 5 10 15
168 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
169 20 25 30
172 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
173 35 40 45
176 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
177 50 55 60
180 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
181 65 70 75 80
184 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
185 85 90 95
188 Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
189 100 105 110
192 Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
193 115 120 125
196 Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys
197 130 135 140

```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\12112003\J720896.raw

```

200 Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala
201 145          150          155          160
204 Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg
205          165          170          175
208 Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly
209          180          185          190
212 Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala
213          195          200          205
216 Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro
217          210          215          220
220 Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr
221 225          230          235          240
224 His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu
225          245          250          255
228 Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys
229          260          265          270
232 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr
233          275          280          285
236 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn
237          290          295          300
240 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn
241 305          310          315          320
244 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile
245          325          330          335
248 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp
249          340          345          350
252 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
253          355          360          365
256 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
257          370          375          380
260 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
261 385          390          395          400
264 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
265          405          410          415
268 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
269          420          425          430
272 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
273          435          440          445
276 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
277          450          455          460
280 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
281 465          470          475          480
284 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
285          485          490          495
288 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
289          500          505          510
292 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
293          515          520          525
296 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu

```

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TIME: 17:13:14

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\12112003\J720896.raw

```

297      530      535      540
300 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly
301 545      550      555      560
304 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His
305      565      570      575
308 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg
309      580      585      590
312 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser
313      595      600      605
316 Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala
317      610      615      620
320 Tyr Leu Cys Phe Cys Leu Lys Gly Thr Thr Gly Pro Asn Cys Glu Ile
321 625      630      635      640
324 Asn Leu Asp Asp Cys Ala Ser Ser Pro Cys Asp Ser Gly Thr Cys Leu
325      645      650      655
328 Asp Lys Ile Asp Gly Tyr Glu Cys Ala Cys Glu Pro Gly Tyr Thr Gly
329      660      665      670
332 Ser Met Cys Asn Ser Asn Ile Asp Glu Cys Ala Gly Asn Pro Cys His
333      675      680      685
336 Asn Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly Phe Thr Cys Arg Cys
337      690      695      700
340 Pro Glu Gly Tyr His Asp Pro Thr Cys Leu Ser Glu Val Asn Glu Cys
341 705      710      715      720
344 Asn Ser Asn Pro Cys Val His Gly Ala Cys Arg Asp Ser Leu Asn Gly
345      725      730      735
348 Tyr Lys Cys Asp Cys Asp Pro Gly Trp Ser Gly Thr Asn Cys Asp Ile
349      740      745      750
352 Asn Asn Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Gly Thr Cys
353      755      760      765
356 Lys Asp Met Thr Ser Gly Ile Val Cys Thr Cys Arg Glu Gly Phe Ser
357      770      775      780
360 Gly Pro Asn Cys Gln Thr Asn Ile Asn Glu Cys Ala Ser Asn Pro Cys
361 785      790      795      800
364 Leu Asn Lys Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn
365      805      810      815
368 Cys Leu Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro
369      820      825      830
372 Cys Ala Pro Ser Pro Cys Arg Asn Gly Gly Glu Cys Arg Gln Ser Glu
373      835      840      845
376 Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly
377      850      855      860
380 Gln Thr Cys Glu Val Asp Ile Asn Glu Cys Val Leu Ser Pro Cys Arg
381 865      870      875      880
W--> 384 His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys
385      885      890      895
388 Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys
389      900      905      910
392 Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn
393      915      920      925

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/720,896

DATE: 12/16/2003
TIME: 17:13:15

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12112003\J720896.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 891

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10

Error Explanation:

VERIFICATION SUMMARY

DATE: 12/16/2003

PATENT APPLICATION: US/10/720,896

TIME: 17:13:15

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\12112003\J720896.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:29 M:283 W: Missing Blank Line separator, <220> field identifier
L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial sequence
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:32
L:42 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:44 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial sequence
L:44 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:44
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:54 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:3
L:56 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial sequence
L:56 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:56
L:64 M:283 W: Missing Blank Line separator, <220> field identifier
L:65 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:66 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4
L:68 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial sequence
L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:68
L:76 M:283 W: Missing Blank Line separator, <220> field identifier
L:77 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:79 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial sequence
L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:79
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:92 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial sequence
L:92 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:92
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:103 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:104 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:7
L:106 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial sequence
L:106 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:106
L:114 M:283 W: Missing Blank Line separator, <220> field identifier
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:116 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:8
L:118 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial sequence
L:118 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:118
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:128 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:9
L:130 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial sequence
L:130 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:130

L:142 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
E:143 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:10
L:145 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial sequence
L:145 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:145

VERIFICATION SUMMARY

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L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:880